

SCORE Search Results Details for Application 09961086 and Search Result 20080917_142909_us-09-961-086a-1.rup.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 09961086 and Search Result 20080917_142909_us-09-961-086a-1.rup.

[Go Back to previous page](#)

GenCore version 6.2.1
Copyright (c) 1993 - 2008 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2008, 21:56:07 ; Search time 407 Seconds
(without alignments)
3112.639 Million cell updates/sec

Title: US-09-961-086A-1
Perfect score: 3352
Sequence: 1 MSSSNVEVFIPVSQGNTNGF.....MIVIFLTIAYLKLLFLKKYS 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5939836 seqs, 1934112985 residues

Total number of hits satisfying chosen parameters: 5939836

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_13.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3346	99.8	655	1	ABCG2_HUMAN	Q9unq0 homo sapien
2	3346	99.8	655	2	A8K1T5_HUMAN	A8k1t5 homo sapien
3	3225	96.2	655	2	A9UKW2_MACMU	A9ukw2 macaca mula
4	3223.5	96.2	654	1	ABCG2_MACMU	Q5mb13 macaca mula
5	3089	92.2	607	2	Q4W5I3_HUMAN	Q4w5i3 homo sapien
6	2890	86.2	658	2	Q09GP3_CAPHI	Q09gp3 capra hircu
7	2886	86.1	658	2	Q009B1_SHEEP	Q009b1 ovis aries
8	2870	85.6	658	2	A7E3T8_BOVIN	A7e3t8 bos taurus
9	2862	85.4	655	1	ABCG2_BOVIN	Q4gzt4 bos taurus
10	2859	85.3	658	2	Q32PJ1_BOVIN	Q32pj1 bos taurus
11	2849.5	85.0	656	1	ABCG2_PIG	Q8mib3 sus scrofa
12	2789	83.2	655	2	Q38JL0_CANFA	Q38jl0 canis famil
13	2762	82.4	657	1	ABCG2_MOUSE	Q7tms5 mus musculu
14	2754	82.2	657	1	ABCG2_RAT	Q80w57 rattus norv
15	2343	69.9	661	2	Q28BS4_XENTR	Q28bs4 xenopus tro
16	2288	68.3	661	2	A1L2M4_XENLA	A1l2m4 xenopus lae
17	2062	61.5	643	2	Q2Q447_DANRE	Q2q447 danio rerio
18	2042	60.9	655	2	A8IJF9_ONCMY	A8ijf9 oncorhynch
19	1974.5	58.9	631	2	Q4SBP6_TETNG	Q4sbp6 tetraodon n
20	1787.5	53.3	650	2	Q8BKI5_MOUSE	Q8bki5 mus musculu
21	1786.5	53.3	650	1	ABCG3_MOUSE	Q99p81 mus musculu
22	1744.5	52.0	646	2	Q4KM08_RAT	Q4km08 rattus norv
23	1703.5	50.8	646	2	Q68HW7_RAT	Q68hw7 rattus norv
24	1663	49.6	613	2	Q2Q444_DANRE	Q2q444 danio rerio
25	1578.5	47.1	652	2	Q498U1_RAT	Q498u1 rattus norv
26	1473	43.9	634	2	Q08CU5_DANRE	Q08cu5 danio rerio
27	1469	43.8	634	2	Q2Q445_DANRE	Q2q445 danio rerio
28	1423	42.5	618	2	Q2Q446_DANRE	Q2q446 danio rerio
29	1422	42.4	618	2	A2BE75_DANRE	A2be75 danio rerio
30	1373	41.0	544	2	A7S071_NEMVE	A7s071 nematostell
31	1158	34.5	502	2	Q5U314_RAT	Q5u314 rattus norv
32	1038.5	31.0	457	2	Q4RBH3_TETNG	Q4rbh3 tetraodon n
33	1036.5	30.9	354	2	Q4SPA5_TETNG	Q4spa5 tetraodon n
34	940	28.0	1159	2	Q54T02_DICDI	Q54t02 dictyosteli
35	891.5	26.6	646	2	Q38AM7_9TRYP	Q38am7 trypanosoma
36	877	26.2	682	2	Q4DW41_TRYCR	Q4dw41 trypanosoma
37	875	26.1	619	2	A9VA57_MONBE	A9va57 monosiga br
38	872	26.0	645	2	A0CJS8_PARTE	A0cjs8 paramecium
39	870.5	26.0	607	2	Q22MH6_TETTH	Q22mh6 tetrahymena
40	866.5	25.9	827	2	A9UUE4_MONBE	A9uue4 monosiga br
41	864	25.8	1039	2	Q6BIH1_DEBHA	Q6bih1 debaryomyce
42	863.5	25.8	867	2	Q24CW4_TETTH	Q24cw4 tetrahymena
43	863	25.7	645	2	Q6BG61_PARTE	Q6bg61 paramecium
44	862.5	25.7	1006	2	A5DNC5_PICGU	A5dnc5 pichia guil
45	854.5	25.5	680	2	A4HPF5_LEIBR	A4hpf5 leishmania

ALIGNMENTS

RESULT 1

ABCG2_HUMAN

ID ABCG2_HUMAN Reviewed; 655 AA.
AC Q9UNQ0; A0A1W3; Q95374; Q53ZQ1; Q569L4; Q5YLG4; Q86V64; Q8IX16;
AC Q96LD6; Q96TA8; Q9BY73; Q9NUS0;
DT 24-JAN-2001, integrated into UniProtKB/Swiss-Prot.
DT 10-MAY-2005, sequence version 3.
DT 08-APR-2008, entry version 84.
DE ATP-binding cassette sub-family G member 2 (Placenta-specific ATP-
DE binding cassette transporter) (Breast cancer resistance protein)
DE (Mitoxantrone resistance-associated protein) (CD338 antigen) (CDw338).
GN Name=ABCG2; Synonyms=ABCP, BCRP, BCRP1, MXR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), VARIANTS GLU-166 AND SER-208,
RP AND TISSUE SPECIFICITY.
RC TISSUE=Placenta;
RX MEDLINE=99065313; PubMed=9850061;
RA Allikmets R., Schriml L.M., Hutchinson A., Romano-Spica V., Dean M.;
RT "A human placenta-specific ATP-binding cassette gene (ABCP) on
RT chromosome 4q22 that is involved in multidrug resistance.";
RL Cancer Res. 58:5337-5339(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Mammary cancer;
RX MEDLINE=99080071; PubMed=9861027; DOI=10.1073/pnas.95.26.15665;
RA Doyle L.A., Yang W., Abruzzo L.V., Krogmann T., Gao Y., Rishi A.K.,
RA Ross D.D.;
RT "A multidrug resistance transporter from human MCF-7 breast cancer
RT cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:15665-15670(1998).
RN [3]
RP ERRATUM.
RA Doyle L.A., Yang W., Abruzzo L.V., Krogmann T., Gao Y., Rishi A.K.,
RA Ross D.D.;
RL Proc. Natl. Acad. Sci. U.S.A. 96:2569-2569(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Kage K., Tsukahara S., Sugiyama T., Asada S., Ishikawa E., Tsuruo T.,
RA Sugimoto Y.;

RT "Breast cancer resistance protein constitutes a 140-kDa complex as a
 RT homodimer.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RX MEDLINE=21201983; PubMed=11306452;
 RA Komatani H., Kotani H., Hara Y., Nakagawa R., Matsumoto M.,
 RA Arakawa H., Nishimura S.;
 RT "Identification of breast cancer resistant protein/mitoxantrone
 RT resistance/placenta-specific, ATP-binding cassette transporter as a
 RT transporter of NB-506 and J-107088, topoisomerase I inhibitors with an
 RT indolocarbazole structure.";
 RL Cancer Res. 61:2827-2832(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RX MEDLINE=21424790; PubMed=11533706; DOI=10.1038/nm0901-1028;
 RA Zhou S., Schuetz J.D., Bunting K.D., Colapietro A.M., Sampath J.,
 RA Morris J.J., Lagutina I., Grosveld G.C., Osawa M., Nakauchi H.,
 RA Sorrentino B.P.;
 RT "The ABC transporter Bcrp1/ABCG2 is expressed in a wide variety of
 RT stem cells and is a molecular determinant of the side-population
 RT phenotype.";
 RL Nat. Med. 7:1028-1034(2001).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND VARIANTS GLU-166
 RP AND SER-208.
 RC TISSUE=Brain endothelium;
 RX MEDLINE=22959505; PubMed=12958161; DOI=10.1096/fj.02-1131fje;
 RA Zhang W., Mojsilovic-Petrovic J., Andrade M.F., Zhang H., Ball M.,
 RA Stanimirovic D.B.;
 RT "The expression and functional characterization of ABCG2 in brain
 RT endothelial cells and vessels.";
 RL FASEB J. 17:2085-2087(2003).
 RN [8]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND VARIANT LYS-141.
 RA Yoshikawa M., Yabuuchi H., Ikegami Y., Ishikawa T.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 RN [9]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND VARIANT PRO-316.
 RA Sudarikov A., Makarik T., Andreeff M.;
 RT "Cell line K562 resistant to Hoechst 33342.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 RN [10]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS MET-12; LYS-141;
 RP HIS-296 AND THR-528.
 RG SeattleSNPs program for genomic applications;
 RL Submitted (SEP-2006) to the EMBL/GenBank/DDBJ databases.
 RN [11]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2), AND VARIANT

RP LYS-141.
 RC TISSUE=Pancreas, and PNS;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 RN [12]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 198-655 (ISOFORM 1).
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ngl285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [13]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 294-655 (ISOFORM 1).
 RX PubMed=9892175;
 RA Miyake K., Mickley L., Litman T., Zhan Z., Robey R.W., Cristensen B.,
 RA Brangi M., Greenberger L., Dean M., Fojo T., Bates S.E.;
 RT "Molecular cloning of cDNAs which are highly overexpressed in
 RT mitoxantrone-resistant cells: demonstration of homology to ABC

RT transport genes.";
 RL Cancer Res. 59:8-13(1999).
 RN [14]
 RP REVIEW.
 RX MEDLINE=21474438; PubMed=11590207;
 RA Schmitz G., Langmann T., Heimerl S.;
 RT "Role of ABCG1 and other ABCG family members in lipid metabolism.";
 RL J. Lipid Res. 42:1513-1520(2001).
 RN [15]
 RP VARIANTS MET-12 AND LYS-141.
 RX MEDLINE=22106379; PubMed=12111378; DOI=10.1007/s100380200041;
 RA Iida A., Saito S., Sekine A., Mishima C., Kitamura Y., Kondo K.,
 RA Harigae S., Osawa S., Nakamura Y.;
 RT "Catalog of 605 single-nucleotide polymorphisms (SNPs) among 13 genes
 RT encoding human ATP-binding cassette transporters: ABCA4, ABCA7, ABCA8,
 RT ABCD1, ABCD3, ABCD4, ABCE1, ABCF1, ABCG1, ABCG2, ABCG4, ABCG5, and
 RT ABCG8.";
 RL J. Hum. Genet. 47:285-310(2002).
 RN [16]
 RP VARIANTS LEU-431 AND LEU-489.
 RX PubMed=15618737; DOI=10.2133/dmpk.18.212;
 RA Itoda M., Saito Y., Shirao K., Minami H., Ohtsu A., Yoshida T.,
 RA Saijo N., Suzuki H., Sugiyama Y., Ozawa S., Sawada J.;
 RT "Eight novel single nucleotide polymorphisms in ABCG2/BCRP in Japanese
 RT cancer patients administered irinotecan.";
 RL Drug Metab. Pharmacokinet. 18:212-217(2003).
 RN [17]
 RP VARIANTS MET-12; LYS-141; LEU-206 AND TYR-590.
 RX PubMed=12544509; DOI=10.1097/00008571-200301000-00004;
 RA Zamber C.P., Lamba J.K., Yasuda K., Farnum J., Thummel K.,
 RA Schuetz J.D., Schuetz E.G.;
 RT "Natural allelic variants of breast cancer resistance protein (BCRP)
 RT and their relationship to BCRP expression in human intestine.";
 RL Pharmacogenetics 13:19-28(2003).
 RN [18]
 RP EFFECT OF THE VARIANTS MET-12; LYS-141 AND ASN-620 ON TRANSPORT.
 RX PubMed=15838659; DOI=10.1007/s00280-004-0931-x;
 RA Morisaki K., Robey R.W., Oezvegy-Laczka C., Honjo Y., Polgar O.,
 RA Steadman K., Sarkadi B., Bates S.E.;
 RT "Single nucleotide polymorphisms modify the transporter activity of
 RT ABCG2.";
 RL Cancer Chemother. Pharmacol. 56:161-172(2005).
 RN [19]
 RP SUBCELLULAR LOCATION, GLYCOSYLATION AT ASN-596, AND MUTAGENESIS OF
 RP ASN-418; ASN-557 AND ASN-596.
 RX PubMed=15807535; DOI=10.1021/bi0479858;
 RA Diop N.K., Hrycyna C.A.;
 RT "N-linked glycosylation of the human ABC transporter ABCG2 on
 RT asparagine 596 is not essential for expression, transport activity, or

RT trafficking to the plasma membrane.";
 RL Biochemistry 44:5420-5429(2005).
 RN [20]
 RP MUTAGENESIS OF LYS-86, SUBCELLULAR LOCATION, AND HOMODIMERIZATION.
 RX PubMed:15769853; DOI=10.1242/jcs.01729;
 RA Henriksen U., Gether U., Litman T.;
 RT "Effect of Walker A mutation (K86M) on oligomerization and surface
 RT targeting of the multidrug resistance transporter ABCG2.";
 RL J. Cell Sci. 118:1417-1426(2005).
 RN [21]
 RP MUTAGENESIS OF ARG-482.

Query Match 99.8%; Score 3346; DB 1; Length 655;
 Best Local Similarity 99.8%; Pred. No. 5e-211;
 Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MSSSNVEVFIPVSGQNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE	60
Db	1	MSSSNVEVFIPVSGQNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE	60
Qy	61	KEILSNINGIMKPLGNAILGPTGGGKSSLLDVLAAARKDPSGLSGDVLINGAPRPANFKCN	120
Db	61	KEILSNINGIMKPLGNAILGPTGGGKSSLLDVLAAARKDPSGLSGDVLINGAPRPANFKCN	120
Qy	121	SGYVVQDDVVMGILTVRENLQFSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT	180
Db	121	SGYVVQDDVVMGILTVRENLQFSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT	180
Qy	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSSTANAVLLLLKRMSKQGRTIIF	240
Db	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSSTANAVLLLLKRMSKQGRTIIF	240
Qy	241	SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Db	241	SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Qy	301	DSTAVALNREEDFKATEIIIEPSKQDKPLIEKLAIEYVNSSFYKETKAELHQLSGGEKKKK	360
Db	301	DSTAVALNREEDFKATEIIIEPSKQDKPLIEKLAIEYVNSSFYKETKAELHQLSGGEKKKK	360
Qy	361	ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKNDS	420
Db	361	ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKNDS	420
Qy	421	TGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFGLKLLSDLLP	480
Db	421	TGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFGLKLLSDLLP	480
Qy	481	MTMLPSIIIFTICIVYFMLGLKPKADAFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL	540


```

      | |||||
Db      481 MRMLPSIIFTCIVYFMLGLKPKADAFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
      |||||
Qy      541 MTICFVFMIMFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFPCPLNATGN 600
      |||||
Db      541 MTICFVFMIMFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFPCPLNATGN 600
      |||||
Qy      601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLFLKKYS 655
      |||||
Db      601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLFLKKYS 655

```

RESULT 2

A8K1T5_HUMAN

```

ID      A8K1T5_HUMAN                      Unreviewed;                      655 AA.
AC      A8K1T5;
DT      04-DEC-2007, integrated into UniProtKB/TrEMBL.
DT      04-DEC-2007, sequence version 1.
DT      08-APR-2008, entry version 5.
DE      cDNA FLJ76761, highly similar to Homo sapiens ATP-binding cassette,
DE      sub-family G (WHITE), member 2(ABCG2), mRNA.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Hippocampus;
RA      Wakamatsu A., Yamamoto J., Kimura K., Ishii S., Watanabe K.,
RA      Sugiyama A., Murakawa K., Kaida T., Tsuchiya K., Fukuzumi Y.,
RA      Kumagai A., Oishi Y., Yamamoto S., Ono Y., Komori Y., Yamazaki M.,
RA      Kisu Y., Nishikawa T., Sugano S., Nomura N., Isogai T.;
RT      "NEDO human cDNA sequencing project.";
RL      Submitted (OCT-2007) to the EMBL/GenBank/DDBJ databases.
CC      -!- SIMILARITY: Belongs to the ABC transporter family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AK290000; BAF82689.1; -; mRNA.
DR      RefSeq; NP_004818.2; -.
DR      UniGene; Hs.480218; -.
DR      GeneID; 9429; -.
DR      GO; GO:0005524; F:ATP binding; IEA:InterPro.
DR      GO; GO:0016887; F:ATPase activity; IEA:InterPro.
DR      InterPro; IPR003593; AAA+_ATPase_core.
DR      InterPro; IPR013525; ABC_2_trans.
DR      InterPro; IPR003439; ABC_transp_like.

```


DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 PE 2: Evidence at transcript level;
 KW ATP-binding; Membrane; Nucleotide-binding; Transmembrane; Transport.
 SQ SEQUENCE 655 AA; 72314 MW; A8AF66B96034C5A8 CRC64;

Query Match 99.8%; Score 3346; DB 2; Length 655;
 Best Local Similarity 99.8%; Pred. No. 5e-211;
 Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MSSSNVEVFIPVSQGNNTGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE	60
Db	1	MSSSNVEVFIPVSQGNNTGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE	60
Qy	61	KEILSNINGIMKPLNAILGPTGGGKSSLLDVLAAKDPDPSGLSGDVLINGAPRPANFKCN	120
Db	61	KEILSNINGIMKPLNAILGPTGGGKSSLLDVLAAKDPDPSGLSGDVLINGAPRPANFKCN	120
Qy	121	SGYVVQDDVVMGTLTVRENLFQSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT	180
Db	121	SGYVVQDDVVMGTLTVRENLFQSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT	180
Qy	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRITIF	240
Db	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRITIF	240
Qy	241	SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Db	241	SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Qy	301	DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAIEYVNSSFYKETKAELHQLSGGEKKKK	360
Db	301	DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAIEYVNSSFYKETKAELHQLSGGEKKKK	360
Qy	361	ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKND	420
Db	361	ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKND	420
Qy	421	TGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLLP	480
Db	421	TGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLLP	480
Qy	481	MTMLPSIIFTCIVYFMLGLKPKADAFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL	540
Db	481	MRMLPSIIFTCIVYFMLGLKPKADAFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL	540


```

Qy      541 MTICFVFMFMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFPCPLNATGN 600
          |||
Db      541 MTICFVFMFMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFPCPLNATGN 600

Qy      601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTTIAYLKLLFLKKYS 655
          |||
Db      601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTTIAYLKLLFLKKYS 655

```

RESULT 3

A9UKW2_MACMU

```

ID      A9UKW2_MACMU              Unreviewed;          655 AA.
AC      A9UKW2;
DT      05-FEB-2008, integrated into UniProtKB/TrEMBL.
DT      05-FEB-2008, sequence version 1.
DT      08-APR-2008, entry version 2.
DE      ATP-binding cassette transporter sub-family G member 2.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.

```

```

RA      Nakanishi T., Tsang A., Cheng X., Ross D.D., MacVittie T., Takebe N.;
RT      "cDNA cloning and functional analysis of rhesus monkey ATP-binding
RT      cassette transporter, BCRP/ABCG2.";
RL      Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.

```

```

CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----

```

```

DR      EMBL; AY864772; AAX56948.1; -; mRNA.
DR      InterPro; IPR003593; AAA+ ATPase_core.
DR      InterPro; IPR013525; ABC_2_trans.
DR      InterPro; IPR003439; ABC_transp_like.
DR      Pfam; PF01061; ABC2_membrane; 1.
DR      Pfam; PF00005; ABC_tran; 1.
DR      ProDom; PD000006; ABC_transporter; 1.
DR      SMART; SM00382; AAA; 1.
DR      PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PE      2: Evidence at transcript level;
KW      ATP-binding.
SQ      SEQUENCE 655 AA; 72601 MW; CE1DEABF5C0648DB CRC64;

```

```

Query Match          96.2%; Score 3225; DB 2; Length 655;
Best Local Similarity 96.2%; Pred. No. 4.6e-203;
Matches 630; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

```


Qy	1	MSSSNVEVFIPVSGQNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLSGFLPCRKPVE	60
Db	1	MSSSNVEVFIPMSQENTNGFPPTTSSNDRKAFTEGAVLSFHNICYRVKVSGLFPGRKPVE	60
Qy	61	KEILSNINGIMKPLGNAILGPTGGGKSSLLDVLAAKDPDPSGLSGDVLINGAPRPANFKCN	120
Db	61	KEILSNINGIMKPLGNAILGPTGGGKSSLLDVLAAKDPDPSGLSGDVLINGALRPTNFKCN	120
Qy	121	SGYVVQDDVVMGTLTVRENLFQSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT	180
Db	121	SGYVVQDDVVMGTLTVRENLFQSAALRLPTTMTNHEKNERINRVIQELGLDKVADSKVGT	180
Qy	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSSTANAVLLLLKRMKSQGRTIIF	240
Db	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSSTANAVLLLLKRMKSQGRTIIF	240
Qy	241	SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Db	241	STHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Qy	301	DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAIEYVNSSFFYKETKAELHQLSGGEKKKK	360
Db	301	DSTAVALNREEDFKATEIIEPSKRDPLVEKLAIEYVDSFFYKETKAELHQLSGGEKKKK	360
Qy	361	ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKND	420
Db	361	ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVLGLVIGGIYFGLNND	420
Qy	421	TGIQNRAGVLFFLTNNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFFGLKLLSDLLP	480
Db	421	TGIQNRAGVLFFLTNNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFFGLKLLSDLLP	480
Qy	481	MTMLPSIIFTICIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVSVATLL	540
Db	481	MRMLPSIIFTICIVYFMLGLKPTADAFFIMMFTLMMVAYSASSMALAIAAGQSVSVATLL	540
Qy	541	MTICFVFMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLQGNFCPGLNATGN	600
Db	541	MTICFVFMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLQGNFCPGLNATVN	600
Qy	601	NPCNYATCTGEEYLVKQIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS	655
Db	601	NTCNYATCTGEEYLVKQIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS	655

RESULT 4

ABCG2_MACMU

ID ABCG2_MACMU

Reviewed;

654 AA.

AC Q5MB13;

DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-2005, sequence version 1.
 DT 15-JAN-2008, entry version 25.
 DE ATP-binding cassette sub-family G member 2 (CD338 antigen).
 GN Name=ABCG2;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
 RC TISSUE=Kidney;
 RX PubMed=15516692; DOI=10.1074/jbc.M409796200;
 RA Ueda T., Brenner S., Malech H.L., Langemeijer S.M., Perl S., Kirby M.,
 RA Phang O.A., Krouse A.E., Donahue R.E., Kang E.M., Tisdale J.F.;
 RT "Cloning and functional analysis of the rhesus macaque ABCG2 gene.
 RT Forced expression confers an SP phenotype among hematopoietic stem
 RT cell progeny in vivo.";
 RL J. Biol. Chem. 280:991-998(2005).
 CC -!- FUNCTION: Xenobiotic transporter that may play an important role
 CC in the exclusion of xenobiotics from the brain. May be involved in
 CC brain-to-blood efflux (By similarity). When overexpressed, the
 CC transfected cells become resistant to mitoxantrone. Overexpression
 CC in bone marrow stem cells does not interfere with hematopoietic
 CC stem cell maturation and increases the number of SP cells.
 CC -!- SUBUNIT: Monomer or homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
 CC (By similarity).
 CC -!- SIMILARITY: Belongs to the ABC transporter family. ABCG (White)
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 ABC transporter domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY841878; AAW28901.1; -; mRNA.
 DR RefSeq; NP_001028091.1; -.
 DR UniGene; Mmu.3144; -.
 DR Ensembl; ENSMUG00000008797; Macaca mulatta.
 DR GeneID; 574307; -.
 DR GO; GO:0005886; C:plasma membrane; IEA:UniProtKB-SubCell.
 DR InterPro; IPR003593; AAA+_ATPase_core.
 DR InterPro; IPR013525; ABC_2_trans.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.

http://es.ScoreAccessWeb/GetItem.action?AppId=099610...7_142909_us-09-961-086a-1.rup&ItemType=4&startByte=0 (13 of 40)9/22/2008 12:01:40 PM

http://es/ScoreAccessWeb/GetItem.action?AppId=099610...7_142909_us-09-961-086a-1.rup&ItemType=4&startByte=0 (14 of 40)9/22/2008 12:01:40 PM

Query Match 92.2%; Score 3089; DB 2; Length 607;
Best Local Similarity 99.8%; Pred. No. 3.6e-194;
Matches 606; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSSSNVEVFIPVSGQNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKFVE 60
 |||||
Db 1 MSSSNVEVFIPVSGQNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKFVE 60

Qy 61 KEILSNINGIMKPLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
 |||||
Db 61 KEILSNINGIMKPLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120


```

Qy      121  SGYVVQDDVVMGILTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT 180
        |||
Db      121  SGYVVQDDVVMGILTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy      181  QFIRGVSGGERKRTSIGMELITDPSILFLEPTTGLDSSSTANAVLLLLKRMSKQGRTIIF 240
        |||
Db      181  QFIRGVSGGERKRTSIGMELITDPSILFLEPTTGLDSSSTANAVLLLLKRMSKQGRTIIF 240

Qy      241  SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
        |||
Db      241  SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy      301  DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
        |||
Db      301  DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy      361  ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKND 420
        |||
Db      361  ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKND 420

Qy      421  TGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLLP 480
        |||
Db      421  TGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLLP 480

Qy      481  MTMLPSIIFTICIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVSVATLL 540
        |
Db      481  MRMLPSIIFTICIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVSVATLL 540

Qy      541  MTICVFMMMFISGLLVNLTIIASWSLWLYFSIPRYGFTALQHNEFLGQNFPCPLNATGN 600
        |||
Db      541  MTICVFMMMFISGLLVNLTIIASWSLWLYFSIPRYGFTALQHNEFLGQNFPCPLNATGN 600

Qy      601  NPCNYAT 607
        |||||
Db      601  NPCNYAT 607

```

RESULT 6

Q09GP3_CAPHI

ID Q09GP3_CAPHI Unreviewed; 658 AA.

AC Q09GP3;

DT 17-OCT-2006, integrated into UniProtKB/TrEMBL.

DT 17-OCT-2006, sequence version 1.

DT 08-APR-2008, entry version 12.

DE ATP-binding cassette sub-family G member 2.

GN Name=ABCG2;

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Wu H., Luo J., Zhang L.;
 RT "Cloning and sequence analyses of ABCG2 gene differentially expressed
 RT in mammary gland at two lactation stages of Xinong Saanen goat.";
 RL Submitted (AUG=2006) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; DQ904356; ABI73985.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.
 DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
 DR GO; GO:0016887; F:ATPase activity; IEA:InterPro.
 DR GO; GO:0006810; P:transport; IEA:UniProtKB-KW.
 DR InterPro; IPR003593; AAA+ATPase_core.
 DR InterPro; IPR013525; ABC_2_trans.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 PE 2: Evidence at transcript level;
 KW ATP-binding; Membrane; Nucleotide-binding; Transmembrane; Transport.
 SQ SEQUENCE 658 AA; 73200 MW; C8BD65DF4E877D62 CRC64;

Query Match 86.2%; Score 2890; DB 2; Length 658;
 Best Local Similarity 85.2%; Pred. No. 5e-181;
 Matches 559; Conservative 43; Mismatches 52; Indels 2; Gaps 2;

Qy 1 MSSSNVEVFIPVSGQNGINGFPATASNDLKAFTEGAVLSFHNICYRVKLSGFLPCRKPVE 60
 |||:: || ||::|: || | | | ||: |||||:::||||:|:|||| ||| :|
 Db 4 MSSNSYEVCIPMSK-KPNGIPETTSKDLQTLTEGAVLSFHDICYRVKVKTGFLLCRKRTIE 62
 Qy 61 KEILSNINGIMKPLGNAILGPTGGGKSSLLDLVAARKDPSGLSGDVLINGAPRPANFKCN 120
 ||||:||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 63 KEILANINGVMKPLGNAILGPTGGGKSSLLDILAARKDPHGLSGDVLINGAPRPANFKCN 122
 Qy 121 SGYVVQDDVVMGILTVRENLOFSAAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 123 SGYVVQDDVVMGILTVRENLOFSAAALRLPTMTNIEKNERINKVIQELGLDKVADSKVGT 182
 Qy 181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRITIF 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 243 SIHQPRYSIFKFLFDSLTLTLLASGRLMFHGPAQEALGYFEDIGFHCEPYNPNADFFLDIING 302

Qy 301 DSTAVALNREE-DFKATEIIIEPSKQDKPLIEKLAIEYVNSSFYKETKAELHQLSGGEKKK 359
||:| |||: | :| | ||| | ||||| ||||:| || | :| || :|

Db 303 DSSAVVLNREDSDEAKETEESKNDTSLIEKLAGFYVNSSFFKETKVELDKFSGERRRK 362

Qy 360 KITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKND 419
|:: :||:| |||||:|:|||||||||||||||:| || |||||: |||

Db 363 KLSYKEITYATSFCHQLKWKISKRSFKNLLGNPQASIAQLIVTVFLGLVIGAIIFYDLKND 422

Qy 420 STGIQNRAGVLFLLTNNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLL 479
:||||||||||||||||| ||||||||||||||| |||||||

Db 423 PSGIQNRAGVLFLLTNNQCFSSVSAVELLVVEKKLFIHEYISGYRVSSYFFGKLLSDLL 482

Qy 480 PMTMLPSIIFTTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVSVATL 539
|| ||||| ||: ||||| :||:|||||||||||||||||: |||

Db 483 PMRMLPSIIFTTCITYFLGLKPKVEAFFIMMFTLMMVAYSASSMALAIAAGQSVVSIATL 542

Qy 540 LMTICFVFMFMIFSGLLVNLTTIASWLSWLQYFSIPRYGTALQHNEFLGQNFPCPLNATG 599
||| ||||| ||||| || :||| ||||: ||||| ||||| ||||| ||

Db 543 LMTISFVFMFMIFSGLLVNLKTIGAWLSWLQYLSIPRYGYAALQHNEFLGQNFPCPLNVTA 602

Qy 600 NNPNCYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
|| |:| ||||:| |||:||||||||||||||||| |||||:|

Db 603 NNTCSYAICTGEEFLTNQGIDISPWGLWKNHVALACMIVIFLTIAYLKLLFLKKFS 658

RESULT 8

A7E3T8_BOVIN

ID A7E3T8_BOVIN Unreviewed; 658 AA.

AC A7E3T8;

DT 11-SEP-2007, integrated into UniProtKB/TrEMBL.

DT 11-SEP-2007, sequence version 1.

DT 08-APR-2008, entry version 7.

DE ATP-binding cassette, sub-family G, member 2.

GN Name=ABCG2;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Pooled;

RX MEDLINE=22135956; PubMed=12140684; DOI=10.1007/s00335-001-2145-4;

RA Sonstegard T.S., Capuco A.V., White J., Van Tassell C.P., Connor E.E.,

RA Cho J., Sultana R., Shade L., Wray J.E., Wells K.D., Quackenbush J.;

RT "Analysis of bovine mammary gland EST and functional annotation of the

RT Bos taurus gene index.";

RL Mamm. Genome 13:373-379(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled;
 RX PubMed=16305752; DOI=10.1186/1471-2164-6-166;
 RA Harhay G.P., Sonstegard T.S., Keele J.W., Heaton M.P., Clawson M.L.,
 RA Snelling W.M., Wiedmann R.T., Van Tassell C.P., Smith T.P.L.;
 RT "Characterization of 954 bovine full-CDS cDNA sequences.";
 RL BMC Genomics 6:166-166(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled;
 RA Harhay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.L.,
 RA Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
 RL Submitted (JUL-2007) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; BT030709; ABS45025.1; -; mRNA.
 DR UniGene; Bt.51973; -.
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.
 DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
 DR GO; GO:0016887; F:ATPase activity; IEA:InterPro.
 DR GO; GO:0006810; P:transport; IEA:UniProtKB-KW.
 DR InterPro; IPR003593; AAA+_ATPase_core.
 DR InterPro; IPR013525; ABC_2_trans.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 PE 2: Evidence at transcript level;
 KW ATP-binding; Membrane; Nucleotide-binding; Transmembrane; Transport.
 SQ SEQUENCE 658 AA; 73078 MW; A3D553463BB294DD CRC64;

Query Match 85.6%; Score 2870; DB 2; Length 658;
 Best Local Similarity 84.5%; Pred. No. 1e-179;
 Matches 554; Conservative 45; Mismatches 55; Indels 2; Gaps 2;

Qy 1 MSSSNVEVFIPVSGQNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
 |||:: || ||:|: || | | | ||: ||||| |||||::|: || | | :|
 Db 4 MSSNSYEVSIPMSK-KLNGIPETTSKDLQTLTEGAVLSFHNICYRVKVTGFLLCRKTIIE 62
 Qy 61 KEILSNINGIMKPLNAILGPTGGGKSSLLDLVAARKDPHGLSGDVLINGAPRPANFKCN 120
 ||||:||||:||||| ||||| |||||: ||||| ||||| ||||| |||||
 Db 63 KEILANINGVMKPLNAILGPTGGGKSSLLDILAARKDPHGLSGDVLINGAPRPANFKCN 122


```

Qy      121  SGYVVQDDVVMGILTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT  180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      123  SGYVVQDDVVMGILTVRENLFQSAALRLPTTMTSYEKNERINKVIQELGLDKVADSKVGT  182

Qy      181  QFIRGVSGGERKRTSIGMELITDPSILFDEPTTGLDSSSTANAVLLLLKRMSKQGRTIIF  240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      183  QFIRGVSGGERKRTSIAMELITDPSILFDEPTTGLDSSSTANAVLLLLKRMSKQGRTIIF  242

Qy      241  SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNPADFFLDIING  300
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      243  SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFGAIGFHCEPYNNPADFFLDIING  302

Qy      301  DSTAVALNREE-DFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETAELHQLSGGEKKK  359
        ||:| |||:  :| | |||:| |||||:|||||:|||||:| || : || :||
Db      303  DSSAVVLNREDIGDEANETEEPSKKDTPLIEKLAEFYVNSSFYKETAELHQLSGGEKKK  362

Qy      360  KITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKND  419
        |:  :||:| |||||:|:|:|||||:|||||:|||||:| ||| |||||:| |||
Db      363  KLPYSYKEVTYATSFCHQLKWSRRSFKNLLGNPQASIAQLIVTVFLGLVIGAIYFGLKND  422

Qy      420  STGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLL  479
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      423  PAGIQNRAGVLFLLTTNQCFSSVSAVELLVVEKKLFIHEYISGYRVSSYFFGKLLSDLL  482

Qy      480  PMTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVSVATL  539
        || ||||| |||:||||| :||:| |||||:|||||:|||||:|||||:|||||:
Db      483  PMRMLPSIIFTCITYFLLGLKPKVEAFFIMMLTLMMVAYSASSMALAIAAGQSVSVIATL  542

Qy      540  LMTICFVFMIFSGLLVNLTTIASWSLWLQYFSIPRYGFTALQHNEFLGQNFPCPLNATG  599
        |||| ||||| |||||: ||||| |||||: |||||:|||||:|||||:|||||:
Db      543  LMTISFVFMIFSGLLVNLKTVPWLSWLQYLSIPRYGYAALQHNEFLGQNFPCPLNVTT  602

Qy      600  NNPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLFLKKYS  655
        || |:| |||||:| |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      603  NNTCSYAICTGEEFLTQNGIDISPWGLWKNHVALACMIVIFLTIAYLKLFLKKFS  658

```

RESULT 9

ABCG2_BOVIN

```

ID  ABCG2_BOVIN              Reviewed;              655 AA.
AC  Q4GZT4;
DT  27-JUN-2006, integrated into UniProtKB/Swiss-Prot.
DT  27-JUN-2006, sequence version 2.
DT  15-JAN-2008, entry version 24.
DE  ATP-binding cassette sub-family G member 2 (CD338 antigen).
GN  Name=ABCG2;
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT SER-578.
 RC STRAIN=Holstein;
 RX PubMed=15998908; DOI=10.1101/gr.3806705;
 RA Cohen-Zinder M., Seroussi E., Larkin D.M., Loo J.J.,
 RA Everts-van der Wind A., Lee J.-H., Drackley J.K., Band M.R.,
 RA Hernandez A.G., Shani M., Lewin H.A., Weller J.I., Ron M.;
 RT "Identification of a missense mutation in the bovine ABCG2 gene with a
 RT major effect on the QTL on chromosome 6 affecting milk yield and
 RT composition in Holstein cattle.";
 RL Genome Res. 15:936-944(2005).
 CC -!- FUNCTION: Xenobiotic transporter that may play an important role
 CC in the exclusion of xenobiotics from the brain. May be involved in
 CC brain-to-blood efflux (By similarity).
 CC -!- SUBUNIT: Monomer or homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein.
 CC -!- SIMILARITY: Belongs to the ABC transporter family. ABCG (White)
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 ABC transporter domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AJ871176; CAI38796.1; ALT_INIT; Genomic_DNA.
 DR UniGene; Bt.51973; -.
 DR Ensembl; ENSBTAG00000017704; Bos taurus.
 DR GO; GO:0005886; C:plasma membrane; IEA:UniProtKB-SubCell.
 DR InterPro; IPR003593; AAA+ATPase_core.
 DR InterPro; IPR013525; ABC_2_trans.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 PE 3: Inferred from homology;
 KW ATP-binding; Glycoprotein; Membrane; Nucleotide-binding; Polymorphism;
 KW Transmembrane; Transport.
 FT CHAIN 1 655 ATP-binding cassette sub-family G member
 FT 2.
 FT /FTId=PRO_0000244032.
 FT TOPO_DOM 1 395 Cytoplasmic (Potential).
 FT TRANSMEM 396 416 Potential.
 FT TOPO_DOM 417 428 Extracellular (Potential).
 FT TRANSMEM 429 449 Potential.

FT	TOPO_DOM	450	477	Cytoplasmic (Potential).
FT	TRANSMEM	478	498	Potential.
FT	TOPO_DOM	499	506	Extracellular (Potential).
FT	TRANSMEM	507	527	Potential.
FT	TOPO_DOM	528	535	Cytoplasmic (Potential).
FT	TRANSMEM	536	556	Potential.
FT	TOPO_DOM	557	630	Extracellular (Potential).
FT	TRANSMEM	631	651	Potential.
FT	TOPO_DOM	652	655	Cytoplasmic (Potential).
FT	DOMAIN	36	285	ABC transporter.
FT	NP_BIND	79	86	ATP (Potential).
FT	CARBOHYD	596	596	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	600	600	N-linked (GlcNAc. . .) (Potential).
FT	VARIANT	578	578	Y -> S (polymorphism affecting milk fat and protein concentration).
SQ	SEQUENCE	655 AA;	72725 MW;	8F1AD75742AD236E CRC64;

Query Match 85.4%; Score 2862; DB 1; Length 655;
 Best Local Similarity 84.3%; Pred. No. 3.5e-179;
 Matches 553; Conservative 45; Mismatches 56; Indels 2; Gaps 2;

Qy	1	MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE	60
Db	1	MSSNSYEVSIPMSK-KLNGIPETTSKDLQTLTEGAVLSFHNICYRVKVTGFLLCRKTIE	59
Qy	61	KEILSNINGIMKPLGNAILGPTGGGKSSLLDVLAAKDKPSGLSGDVLINGAPRPANFKCN	120
Db	60	KEILANINGVMKPLGNAILGPTGGGKSSLLDILAARKDPHGLSGDVLINGAPRPANFKCN	119
Qy	121	SGYVVQDDVVMGTLTVRENLFQSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT	180
Db	120	SGYVVQDDVVMGTLTVRENLFQSAALRLPTMTSYEKNERINKVIQELGLDKVADSKVGT	179
Qy	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF	240
Db	180	QFIRGVSGGERKRTSIAMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF	239
Qy	241	SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Db	240	SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFGAIGFRCEPYNPNADFFLDIING	299
Qy	301	DSTAVALNREE-DFKATEIIEPSKQDKPLIEKLAIEYVNSSFYKETKAELHQLSGGEKKK	359
Db	300	DSSAVVLNREDIGDEANETEEPSKKDTPLIEKLAIEFYVNSSFFKETKVELDKFSGDQRRK	359
Qy	360	KITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKND	419
Db	360	KLPSYKEVTYATSFCHQLKWSRSSFKNLLGNPQASIAQLIVTVVLGLVIGAIYFDLKN	419


```

Qy      420 STGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLL 479
      |||
Db      420 PAGIQNRAGVLFLLTTNQCFSSVSAVELLVVEKKLFIHEYISGYRVSSYFFGKLLSDLL 479

Qy      480 PMTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVSVATL 539
      || |||
Db      480 PMRMLPSIIFTCITYFLLGLKPKVEAFFIMMLTLMVAYSASSMALAIAAGQSVVSIATL 539

Qy      540 LMTICFVFMIFSGLLVNLTTIASWSLWLYFSIPRYGFTALQHNEFLGQNFCPGLNATG 599
      ||| |||
Db      540 LMTISFVFMIFSGLLVNLKTVPWLSWLQYLSIPRYGYAALQHNEFLGQNFCPGLNVT 599

Qy      600 NNPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLFLKKYS 655
      || |||
Db      600 NNTCSYAICTGEEFLTQGGIDISPWGLWKNHVALACMIVIFLTIAYLKLFLKKFS 655

```

RESULT 10

Q32PJ1_BOVIN

```

ID      Q32PJ1_BOVIN                      Unreviewed;          658 AA.
AC      Q32PJ1;
DT      06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT      19-SEP-2006, sequence version 2.
DT      08-APR-2008, entry version 36.
DE      ATP-binding cassette, sub-family G (WHITE), member 2.
GN      Name=ABCG2;
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC      Pecora; Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA      Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA      Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA      Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA      Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA      Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA      Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL      Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: Belongs to the ABC transporter family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; BC108097; AAI08098.2; -; mRNA.
DR      RefSeq; NP_001032555.2; -.
DR      UniGene; Bt.51973; -.

```


DR Ensembl; ENSBTAG00000017704; Bos taurus.
 DR GeneID; 536203; -.
 DR KEGG; bta:536203; -.
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.
 DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
 DR GO; GO:0016887; F:ATPase activity; IEA:InterPro.
 DR GO; GO:0006810; P:transport; IEA:UniProtKB-KW.
 DR InterPro; IPR003593; AAA+_ATPase_core.
 DR InterPro; IPR013525; ABC_2_trans.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS05093; ABC_TRANSPORTER_2; 1.
 PE 2: Evidence at transcript level;
 KW ATP-binding; Membrane; Nucleotide-binding; Transmembrane; Transport.
 SQ SEQUENCE 658 AA; 73113 MW; 53DB7AAF29B6202A CRC64;

Query Match 85.3%; Score 2859; DB 2; Length 658;
 Best Local Similarity 84.1%; Pred. No. 5.5e-179;
 Matches 552; Conservative 46; Mismatches 56; Indels 2; Gaps 2;

Qy 1 MSSSNVEVFIPVSGQNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
 |||:: || ||:|: || | | | |:: ||||| |||||::|:| || |:
 Db 4 MSSNSYEVSIIPMSK-KLNGIPETTSKDLQTLTEGAVLSFHNICYRVKVTGFLLCRK TIE 62

Qy 61 KEILSNINGIMKPLGNAILGPTGGGKSSLLDVLAAARKDPSSGLSGDVLINGAPRPANFKCN 120
 |||::|||:||||| |||||::||| ||||| ||||| ||||| |||||
 Db 63 KEILANINGVMKPLGNAILGPTGGGKSSLLDILAARKDPHGLSGDVLINGAPRPANFKCN 122

Qy 121 SGYVVQDDVVMGTLTVRENLFQSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
 ||||| ||||| ||||| ||||| |||||::||| ||||| ||||| |||||
 Db 123 SGYVVQDDVVMGTLTVRENLFQSAALRLPTTMTSYEKNERINKVIQELGLDKVADSKVGT 182

Qy 181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 183 QFIRGVSGGERKRTSIAMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 242

Qy 241 SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 243 SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFGAIGFRCEPYNNPADFFLDIING 302

Qy 301 DSTAVALNREE-DFKATEIIEPSKQDKPLIEKLAIEYVNSSFYKETKAELHQLSGGEKKK 359
 ||:| ||||: :| | ||||:| ||||| |||||:|||| ||: ||::|
 Db 303 DSSAVVLNREDIGDEANETEEPSKKDTPLIEKLAIEFYVNSSFFKETKVELDKFSGDQRRK 362

Qy 360 KITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKND 419
 |: :||::| |||||::|:|:||||| |||||:|||| |||||::| |||

Db 363 KLPSYKEVYATSFCHQLKWSRRSFKNLLGNPQSSIAQLIVTVFLGLVIGAIIFYDLKND 422

Qy 420 STGIQNRAGVLFLLTTNQCFSSVSVAVELFVVEKKLFIHEYISGYRVSYYFLGKLLSDLL 479
 |||

Db 423 PAGIQNRAGVLFLLTTNQCFSSVSVAVELLVVEKKLFIHEYISGYRVSYYFFGKLLSDLL 482

Qy 480 PMTMLPSIIFTTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATL 539
 || |||

Db 483 PMRMLPSIIFTTCITYFLLGLKPKVEAFFIMMLTLMMVAYSASSMALAIAAGQSVVSIATL 542

Qy 540 LMTICFVFMIMIFSGLLVNLTTIASWSLWLYFSIPRYGFTALQHNEFLGQNFPCPLNATG 599
 ||| |||

Db 543 LMTISFVFMIMIFSGLLVNLKTVPWLSWLQYLSIPRYGYAALQHNEFLGQNFPCPLNVTT 602

Qy 600 NNPNCYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLFLKKYS 655
 || |||

Db 603 NNTCSYAICTGEEFLTNQGIDISPWGLWKNHVALACMIVIFLTIAYLKLFLKKFS 658

RESULT 11

ABCG2_PIG

ID ABCG2_PIG Reviewed; 656 AA.

AC Q8MIB3;

DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-2002, sequence version 1.

DT 15-JAN-2008, entry version 31.

DE ATP-binding cassette sub-family G member 2 (Brain multidrug resistance protein) (CD338 antigen).

GN Name=ABCG2; Synonyms=BMDP;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

OC Sus.

OX NCBI_TaxID=9823;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.

RX MEDLINE=22050127; PubMed=12054514; DOI=10.1016/S0006-291X(02)00376-5;

RA Eisenblaetter T., Galla H.-J.;

RT "A new multidrug resistance protein at the blood-brain barrier.";

RL Biochem. Biophys. Res. Commun. 293:1273-1278(2002).

CC -!- FUNCTION: Xenobiotic transporter that may play an important role in the exclusion of xenobiotics from the brain. May be involved in brain-to-blood efflux (By similarity).

CC -!- SUBUNIT: Monomer or homodimer; disulfide-linked (By similarity).

CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein (By similarity).

CC -!- TISSUE SPECIFICITY: High expression in brain, kidney and lung. Also expressed in liver, colon, small intestine, heart, skeletal muscle, spleen, stomach and pancreas.

CC -!- SIMILARITY: Belongs to the ABC transporter family. ABCG (White)
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 ABC transporter domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AJ420927; CAD12785.1; -; mRNA.
 DR PIR; JC7860; JC7860.
 DR RefSeq; NP_999175.1; -.
 DR UniGene; Ssc.64; -.
 DR GeneID; 397073; -.
 DR KEGG; ssc:397073; -.
 DR GO; GO:0005886; C:plasma membrane; IEA:UniProtKB-SubCell.
 DR InterPro; IPR003593; AAA+ATPase_core.
 DR InterPro; IPR013525; ABC_2_trans.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 PE 2: Evidence at transcript level;
 KW ATP-binding; Glycoprotein; Membrane; Nucleotide-binding;
 KW Transmembrane; Transport.
 FT CHAIN 1 656 ATP-binding cassette sub-family G member
 FT 2.
 FT /FTId=PRO_0000093389.
 FT TOPO_DOM 1 394 Cytoplasmic (Potential).
 FT TRANSMEM 395 415 Potential.
 FT TOPO_DOM 416 429 Extracellular (Potential).
 FT TRANSMEM 430 450 Potential.
 FT TOPO_DOM 451 478 Cytoplasmic (Potential).
 FT TRANSMEM 479 498 Potential.
 FT TOPO_DOM 499 507 Extracellular (Potential).
 FT TRANSMEM 508 530 Potential.
 FT TOPO_DOM 531 536 Cytoplasmic (Potential).
 FT TRANSMEM 537 557 Potential.
 FT TOPO_DOM 558 631 Extracellular (Potential).
 FT TRANSMEM 632 652 Potential.
 FT TOPO_DOM 653 656 Cytoplasmic (Potential).
 FT DOMAIN 37 286 ABC transporter.
 FT NP_BIND 80 87 ATP (Potential).
 FT CARBOHYD 597 597 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 601 601 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 656 AA; 72392 MW; 118ADD5B53D9D67F CRC64;

Query Match 85.0%; Score 2849.5; DB 1; Length 656;

Best Local Similarity 84.3%; Pred. No. 2.3e-178;

Matches 553; Conservative 44; Mismatches 58; Indels 1; Gaps 1;

Qy	1	MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLSGFLPCRKPVE	60
Db	1	MSSNSYQVSIPIMSKRNTNGLPGSSSNELKTSAGGAVLSFHDICRYVKVKSGLFLCRKTVE	60
Qy	61	KEILSNINGIMKPLNAILGPTGGGKSSLLDVLAAARKDPSSGLSGDVLINGAPRPANFKCN	120
Db	61	KEILTNINGIMKPLNAILGPTGGGKSSLLDVLAAARKDPHGLSGDVLINGAPRPANFKCN	120
Qy	121	SGYVVQDDVVMGTLTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT	180
Db	121	SGYVVQDDVVMGTLTVRENLFQSAALRLPTMTNHEKNERINMVIQELGLDKVADSKVGT	180
Qy	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMASKQGRTIIF	240
Db	181	QFIRGVSGGERKRTSIAMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMASKQGRTIIF	240
Qy	241	SIHQPRYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Db	241	SIHQPRYSIFKLFDSLTLASGRLMFHGPAAREALGYFASIGYNCEPYNNPADFFLDVING	300
Qy	301	DSTAVALNR-EEDFKATEIIIEPSKQDKPLIEKLAIEIYVNSSFYKETKAELHQLSGGEKKK	359
Db	301	DSSAVVLSRADRDEGAQEPEEPPEKDTPLIDKLAIFYTNSSFFKDTKVELDQFSGGRKKK	360
Qy	360	KITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKND	419
Db	361	KSSVYKEVYTTSFCHQLRWISRRSFKNLLGNPQASVAQIIIVTIILGLVIGAIIFYDLKND	420
Qy	420	STGIQNRAGVLFFLTNTQCFSSVSVAVELFVVEKKLFIHEYISGYRVVSSYFLGKLLSDLL	479
Db	421	PSGIQNRAGVLFFLTNTQCFSSVSVAVELLVVEKKLFIHEYISGYRVVSSYFFGKLLSDLL	480
Qy	480	PMTMLPSIIFTTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATL	539
Db	481	PMRMLPSIIFTTCITYFLGLKPAVGSEFFIMMFTLMMVAYSASSMALAIAAGQSVVSVATL	540
Qy	540	LMTICFVFMFIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFPCPLNATG	599
Db	541	LMTISFVFMFIFSGLLVNLKTVPWLSWLQYFSIPRYGFSALQYNEFLGQNFPCPLNVTT	600
Qy	600	NNPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS	655
Db	601	NNTCSFAICTGAEYLENQGISLSAWGLWQNHVALACMMVIFLTIAYLKLLLLKKYS	656

RESULT 12

Q38JL0_CANFA

ID Q38JL0_CANFA Unreviewed; 655 AA.
 AC Q38JL0;
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 22-NOV-2005, sequence version 1.
 DT 08-APR-2008, entry version 31.
 DE Breast cancer resistance protein.
 GN Name=BCRP;
 OS *Canis familiaris* (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae;
 OC *Canis*.
 OX NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RA Otto A., Gabel G., Honscha K.U.;
 RT "cMXR mediated chemoresistance in canine mammary cancer.";
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; DQ222459; ABB03737.1; -; mRNA.
 DR RefSeq; NP_001041486.1; -.
 DR UniGene; Cfa.9822; -.
 DR Ensembl; ENSCAFG0000009638; *Canis familiaris*.
 DR GeneID; 478472; -.
 DR KEGG; cfa:478472; -.
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.
 DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
 DR GO; GO:0016887; F:ATPase activity; IEA:InterPro.
 DR GO; GO:0006810; P:transport; IEA:UniProtKB-KW.
 DR InterPro; IPR003593; AAA+ATPase_core.
 DR InterPro; IPR013525; ABC_2_trans.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 PE 2: Evidence at transcript level;
 KW ATP-binding; Membrane; Nucleotide-binding; Transmembrane; Transport.
 SQ SEQUENCE 655 AA; 72718 MW; 0C2E9EDBE0A07DF3 CRC64;

Query Match 83.2%; Score 2789; DB 2; Length 655;
 Best Local Similarity 82.7%; Pred. No. 2.2e-174;
 Matches 544; Conservative 48; Mismatches 60; Indels 6; Gaps 3;

Qy	1	MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE	60
		: : : :	
Db	1	MSSNNDPVCIPMSQSRSTNDLSRMTSNDLKTSTEVAVLSFHNIYYRVKVKSGFLGRKTVE	60
Qy	61	KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAAARKDPSGLSGDVLINGAPRPANFKCN	120
		: : :	
Db	61	KEILTNINGVMRPGLNAILGPTGGGKSSLLDVLAAARKDPHGLSGDVLINGAPRPANFKCN	120
Qy	121	SGYVVQDDVVMGTLTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT	180
Db	121	SGYVVQDDVVMGTLTVRENLFQSAALRLPTTTTSHEKNERINKVQQQLGLDKVADSKVGT	180
Qy	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF	240
Db	181	QFIRGVSGGERKRTSIGMELITDPAILFLDEPTTGLDSSTANAVLLLLKRMSEQGRTIIF	240
Qy	241	SIHQPRYSIFKFLDSTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING	300
Db	241	SIHQPRYSIFKFLDSTLLAAGKLMFHGPAQEALGFFASVGYHCEPYNNPADFFLDVING	300
Qy	301	DSTAVALNREE---DFKATEIIEPSKQDKPLIEKLAIEYVNSSFYKETKAELHQLSGGEK	357
		: : : : : :	
Db	301	DSSAVVLNREDQEGEVKYTE--EPSKRGTPFIERIAEFYANSDFCRKTKEELDQLSKSQK	358
Qy	358	KKKITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLK	417
		: : : : :	
Db	359	RKS-SAFKEITYATSFCCQLKWISKRSFKNLLGNPQASIAQIIVTVILGLVLGAIFYDLK	417
Qy	418	NDSTGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSD	477
		:	
Db	418	NDSTGIQNRSGVLFLLTTNQCFSSVSAVELLVVEKKLFIHEYISGYRVSSYFFGKLLSD	477
Qy	478	LLPMTMLPSIIFTCIVFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVA	537
		: : :	
Db	478	LLPMRMLPSIIFTCIIFLLGLKPVVEAFFIMFTLMMVAYSASSMALAIAAGQSVVSIA	537
Qy	538	TLLMTICFVFMFISGLLVNLTIIASWSLWQYFSIPRYGFTALQHNEFLGQNFPCPLNA	597
		:	
Db	538	TLLMTITVFMMFISGLLVNLRVTGVPWLSWLQYLSIPRYGYAALQYNEFLGQNFPCGVNV	597
Qy	598	TGNNPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS	655
		: : : : : : : : : :	
Db	598	TTNNTCSYAICTGEEFLNQGIELSPWGLWKNHVALGCMIVIFLTIAYLKLLFLKKYS	655

RESULT 13

ABCG2_MOUSE

ID ABCG2_MOUSE

Reviewed;

657 AA.

AC Q7TMS5; Q9R004; Q9Z1T0;
 DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2003, sequence version 1.
 DT 08-APR-2008, entry version 43.
 DE ATP-binding cassette sub-family G member 2 (Breast cancer resistance
 DE protein 1 homolog) (CD338 antigen).
 GN Name=Abcg2; Synonyms=Abcp, Bcrp1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
 RC STRAIN=FVB; TISSUE=Liver;
 RX MEDLINE=99413474; PubMed=10485464;
 RA Allen J.D., Brinkhuis R.F., Wijnholds J., Schinkel A.H.;
 RT "The mouse Bcrp1/Mxr/Abcp gene: amplification and overexpression in
 RT cell lines selected for resistance to topotecan, mitoxantrone, or
 RT doxorubicin.";
 RL Cancer Res. 59:4237-4241(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic stem cell;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 511-657.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=99065313; PubMed=9850061;
 RA Allikmets R., Schriml L.M., Hutchinson A., Romano-Spica V., Dean M.;
 RT "A human placenta-specific ATP-binding cassette gene (ABCP) on
 RT chromosome 4q22 that is involved in multidrug resistance.";
 RL Cancer Res. 58:5337-5339(1998).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20493324; PubMed=11036110; DOI=10.1093/jnci/92.20.1651;
 RA Jonker J.W., Smit J.W., Brinkhuis R.F., Maliepaard M., Beijnen J.H.,
 RA Schellens J.H., Schinkel A.H.;
 RT "Role of breast cancer resistance protein in the bioavailability and
 RT fetal penetration of topotecan.";
 RL J. Natl. Cancer Inst. 92:1651-1656(2000).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=21424790; PubMed=11533706; DOI=10.1038/nm0901-1028;
 RA Zhou S., Schuetz J.D., Bunting K.D., Colapietro A.M., Sampath J.,

RA Morris J.J., Lagutina I., Grosveld G.C., Osawa M., Nakauchi H.,
RA Sorrentino B.P.;
RT "The ABC transporter Bcrp1/ABCG2 is expressed in a wide variety of
RT stem cells and is a molecular determinant of the side-population
RT phenotype.";
RL Nat. Med. 7:1028-1034(2001).
CC -!- FUNCTION: Xenobiotic transporter that may play an important role
CC in the exclusion of xenobiotics from the brain. May be involved in
CC brain-to-blood efflux (By similarity). May play a role in early
CC stem cell self-renewal by blocking differentiation.
CC -!- SUBUNIT: Monomer or homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
CC (By similarity).
CC -!- TISSUE SPECIFICITY: Highly expressed in kidney. Lower expression
CC in liver, colon, heart, spleen, and placenta.
CC -!- SIMILARITY: Belongs to the ABC transporter family. ABCG (White)
CC subfamily.
CC -!- SIMILARITY: Contains 1 ABC transporter domain.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF140218; AAD54216.1; -; mRNA.
DR EMBL; BC053730; AAH53730.1; -; mRNA.
DR EMBL; AF103875; AAD09189.1; -; mRNA.
DR RefSeq; NP_036050.1; -.
DR UniGene; Mm.333096; -.
DR PhosphoSite; Q7TMS5; -.
DR Ensembl; ENSMUSG00000029802; Mus musculus.
DR GeneID; 26357; -.
DR KEGG; mmu:26357; -.
DR MGI; MGI:1347061; Abcg2.
DR ArrayExpress; Q7TMS5; -.
DR GermOnline; ENSMUSG00000029802; Mus musculus.
DR InterPro; IPR003593; AAA+ATPase_core.
DR InterPro; IPR013525; ABC_2_trans.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF01061; ABC2_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PE 2: Evidence at transcript level;
KW ATP-binding; Glycoprotein; Membrane; Nucleotide-binding;
KW Transmembrane; Transport.
FT CHAIN 1 657 ATP-binding cassette sub-family G member
FT 2.
FT /FTId=PRO_0000093388.

FT	TOPO_DOM	1	393	Cytoplasmic (Potential).
FT	TRANSMEM	394	414	Potential.
FT	TOPO_DOM	415	428	Extracellular (Potential).
FT	TRANSMEM	429	449	Potential.
FT	TOPO_DOM	450	477	Cytoplasmic (Potential).
FT	TRANSMEM	478	498	Potential.
FT	TOPO_DOM	499	506	Extracellular (Potential).
FT	TRANSMEM	507	527	Potential.
FT	TOPO_DOM	528	535	Cytoplasmic (Potential).
FT	TRANSMEM	536	556	Potential.
FT	TOPO_DOM	557	632	Extracellular (Potential).
FT	TRANSMEM	633	653	Potential.
FT	TOPO_DOM	654	657	Cytoplasmic (Potential).
FT	DOMAIN	48	285	ABC transporter.
FT	NP_BIND	79	86	ATP (Potential).
FT	CARBOHYD	596	596	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	600	600	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	23	23	T -> M (in Ref. 1; AAD54216).
FT	CONFLICT	492	492	V -> I (in Ref. 1; AAD54216).
FT	CONFLICT	512	516	TLIMV -> GLGAE (in Ref. 3).
SQ	SEQUENCE	657 AA;	72978 MW;	DCD70C5D9FA2BA5F CRC64;

Query Match 82.4%; Score 2762; DB 1; Length 657;
 Best Local Similarity 81.5%; Pred. No. 1.3e-172;
 Matches 536; Conservative 52; Mismatches 66; Indels 4; Gaps 3;

Qy	1	MSSSNVEVFIPVSQGNTEGFPATASNDLKAFTEGAVLSFHNICYRVKLSGFLPCRKPVE	60
Db	1	MSSSDHVLVPMSPQRNNGLPRTNSRAVRTLAEGDVLFSHHITYRVKVKSGFL-VRKTV	59
Qy	61	KEILSNINGIMKPLGNAILGPTGGGKSSLLDVLAAKDPKSGLDVINGAPRPAHFKN	120
Db	60	KEILSDINGIMKPLGNAILGPTGGGKSSLLDVLAAKDPKGLSGDVINGAPQPAHFKCC	119
Qy	121	SGYVVQDDVVMGTLTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGT	180
Db	120	SGYVVQDDVVMGTLTVRENLFQSAALRLPTTMKNHEKNERINTIIKELGLEKLVADSKVGT	179
Qy	181	QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF	240
Db	180	QFIRGISGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF	239
Qy	241	SIHQPRYSIFKLFDSLTLLASGRMLFHGPAQAEALGYFESAGYHCEAYNNPADFFLDIING	300
Db	240	SIHQPRYSIFKLFDSLTLLASGKLVFHGPAQKALEYFASAGYHCEPYNNPADFFLDVING	299
Qy	301	DSTAVALNREE-DFKATEIIEPSKQDKPLIEKLAIEIVNSSFYKETAELHQLSGGEKKK	359
Db	300	DSSAVMLNREEQDNEANKTEEPSKGEKPVIEINLSEFYINSAYGETKAELDQLPGAQEKK	359


```

Qy      360 KITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKND 419
      : ||| | | |||||:::|||||||:|:|:|:|:|:| | |
Db      360 GTSAFKEPVYVTSFCHQLRWIARRSFKNLLGNPQASVAQLIVTVILGLIIGAIYFDLKYD 419

Qy      420 STGIQNRAGVLFFLTNNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLL 479
      : |:|||||:|||||:|||||:|||||:|||||:|||||:|:|:|
Db      420 AAGMQNRAGVLFFLTNNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFFGKVMSDL 479

Qy      480 PMTMLPSIIFTTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVSVSATL 539
      || |||:|:|:|:| |||:|:|:|:|:|:|:|:|:|:|:|
Db      480 PMRFLPSVIFTCVLYFMLGLKKTVDAFFIMFTLIMVAYTASSMALAIATGQSVSVSATL 539

Qy      540 LMTICFVFMFMIFSGLLVNLTTIASWSLWLYFSIPRYGFTALQHNEFLGQNEFCPLNATG 599
      ||| ||||:|:|:| || |||||:|:|:|:|:|:|:|:| ||| |
Db      540 LMTIAFVFMMLFSGLLVNLRTIGPWLSWLQYFSIPRYGFTALQYNEFLGQEFPGFNVT 599

Qy      600 NNPC--NYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLFLKKYS 655
      |: | :|| || |:| |:|:|:|:|:|:|:|:|:|:|:|
Db      600 NSTCVNSYAICTGNEYLINQGIELSPWGLWKNHVALACMIIIFLTIAYLKLFLKKYS 657

```

RESULT 14

ABCG2_RAT

```

ID      ABCG2_RAT                      Reviewed;          657 AA.
AC      Q80W57; Q80ST1; Q80UR3; Q80XF3;
DT      21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT      01-JUN-2003, sequence version 1.
DT      08-APR-2008, entry version 39.
DE      ATP-binding cassette sub-family G member 2 (Breast cancer resistance
DE      protein 1 homolog) (CD338 antigen).
GN      Name=Abcg2; Synonyms=Bcrp1;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidea; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RX      PubMed=12819005;
RA      Shimano K., Satake M., Okaya A., Kitanaka J., Kitanaka N.,
RA      Takemura M., Sakagami M., Terada N., Tsujimura T.;
RT      "Hepatic oval cells have the side population phenotype defined by
RT      expression of ATP-binding cassette transporter ABCG2/BCRP1.";
RL      Am. J. Pathol. 163:3-9(2003).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [MRNA], GLYCOSYLATION, SUBCELLULAR LOCATION, AND
RP      TISSUE SPECIFICITY.
RC      STRAIN=Wistar; TISSUE=Brain capillary;

```



```

RX PubMed=15255930; DOI=10.1111/j.1471-4159.2004.02537.x;
RA Hori S., Ohtsuki S., Tachikawa M., Kimura N., Kondo T., Watanabe M.,
RA Nakashima E., Terasaki T.;
RT "Functional expression of rat ABCG2 on the luminal side of brain
RT capillaries and its enhancement by astrocyte-derived soluble
RT factor(s).";
RL J. Neurochem. 90:526-536(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RA Yabuuchi H., Ishikawa T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 506-657.
RC STRAIN=Sprague-Dawley; TISSUE=Brain endothelium;
RA Zhang W., Stanimirovic D.B.;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Xenobiotic transporter that may play an important role
CC in the exclusion of xenobiotics from the brain. May be involved in
CC brain-to-blood efflux (By similarity).
CC -!- SUBUNIT: Monomer or homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
CC (By similarity).
CC -!- TISSUE SPECIFICITY: Highly expressed in brain capillary, kidney
CC and small intestine. Lower expression in heart. Preferentially
CC expressed (at protein level) on the luminal membrane of brain
CC capillaries, in kidney and small intestine.
CC -!- PTM: N-glycosylated in brain capillary, kidney and small intestine
CC but not in heart.
CC -!- SIMILARITY: Belongs to the ABC transporter family. ABCG (White)
CC subfamily.
CC -!- SIMILARITY: Contains 1 ABC transporter domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB094089; BAC75666.1; -; mRNA.
DR EMBL; AB105817; BAC76396.1; -; mRNA.
DR EMBL; AY089996; AAM09106.1; -; mRNA.
DR EMBL; AY089997; AAM09107.1; -; mRNA.
DR EMBL; AY089998; AAM09108.1; -; mRNA.
DR EMBL; AY274118; AAP23237.1; -; mRNA.
DR RefSeq; NP_852046.1; -.
DR UniGene; Rn.13131; -.
DR Ensembl; ENSRNOG0000007041; Rattus norvegicus.
DR GeneID; 312382; -.
DR KEGG; rno:312382; -.
DR RGD; 631345; Abcg2.
DR ArrayExpress; Q80W57; -.

```


DR GermOnline; ENSRNOG00000007041; Rattus norvegicus.
 DR GO; GO:0005886; C:plasma membrane; IEA:UniProtKB-SubCell.
 DR InterPro; IPR003593; AAA+_ATPase_core.
 DR InterPro; IPR013525; ABC_2_trans.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF01061; ABC2_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 PE 1: Evidence at protein level;
 KW ATP-binding; Glycoprotein; Membrane; Nucleotide-binding;
 KW Transmembrane; Transport.
 FT CHAIN 1 657 ATP-binding cassette sub-family G member
 FT 2.
 FT /FTId=PRO_0000093390.
 FT TOPO_DOM 1 395 Cytoplasmic (Potential).
 FT TRANSMEM 396 416 Potential.
 FT TOPO_DOM 417 428 Extracellular (Potential).
 FT TRANSMEM 429 449 Potential.
 FT TOPO_DOM 450 477 Cytoplasmic (Potential).
 FT TRANSMEM 478 498 Potential.
 FT TOPO_DOM 499 506 Extracellular (Potential).
 FT TRANSMEM 507 527 Potential.
 FT TOPO_DOM 528 535 Cytoplasmic (Potential).
 FT TRANSMEM 536 556 Potential.
 FT TOPO_DOM 557 632 Extracellular (Potential).
 FT TRANSMEM 633 653 Potential.
 FT TOPO_DOM 654 657 Cytoplasmic (Potential).
 FT DOMAIN 48 285 ABC transporter.
 FT NP_BIND 79 86 ATP (Potential).
 FT CARBOHYD 596 596 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 600 600 N-linked (GlcNAc . . .) (Potential).
 FT CONFLICT 363 365 AFR -> PFK (in Ref. 1; BAC75666).
 FT CONFLICT 431 431 F -> L (in Ref. 1; BAC75666).
 FT CONFLICT 492 492 I -> L (in Ref. 3; AAM09106/AAM09107/
 FT AAM09108).
 FT CONFLICT 502 502 T -> L (in Ref. 1; BAC75666).
 FT CONFLICT 510 510 M -> R (in Ref. 1; BAC75666).
 SQ SEQUENCE 657 AA; 72961 MW; C975C61A08489027 CRC64;

Query Match 82.2%; Score 2754; DB 1; Length 657;
 Best Local Similarity 81.0%; Pred. No. 4.4e-172;
 Matches 533; Conservative 52; Mismatches 69; Indels 4; Gaps 3;

Qy 1 MSSSNVEVFIPVSQGNTEGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
 ||||| | :|:| | | | : | : | |||||:| |||:|||| | | |
 Db 1 MSSSDNHVLVPMSSQRNKNGLPGMSSRGARTLAEGDVLSEFHIIITYRVKVKSGFL-VRKTAE 59

http://es.ScoreAccessWeb/GetItem.action?AppId=099610...7_142909_us-09-961-086a-1.rup&ItemType=4&startByte=0 (38 of 40)9/22/2008 12:01:40 PM

Query Match 69.9%; Score 2343; DB 2; Length 661;
Best Local Similarity 69.2%; Pred. No. 4.8e-145;
Matches 456; Conservative 81; Mismatches 102; Indels 20; Gaps 5;

Qy 6 VEVFIPVSGQNTNGFPATASNDLKAFTEGAVLSFHNICYRVKCLKSGLFLPCRKPVEKEILS 65
|:: | | | | | | | | | | | | | : | | | : | |
Db 10 VQILDPTVNGEVK-----KKGRKKTLSGAVLSFYNNINYKVVKVKSGLICCRKVTERVILN 63

Qv 66 NINGIMKPGLNAILGPTGGGKSSLLDVLAAARKDPSPGLSGDVLINGAPRPNANFKCNSGYVV 125


```

      ::|||
Db      64 DVNGIMKPLGNAILGPTSGKSSLLDVLAAKDPNGLSGQVLVDGEPQPSNFKCLSGYV 123

Qy      126 QDDVVMGTLTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVADSKVGTQFIR 185
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      124 QDDVVMGTLISIRENLQFSAALRLPRSVKQKEKDERINQVIKELGLTKVADSKVGTQFIR 183

Qy      186 VSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMASKGRTIIFSIHQ 245
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      184 VSGGERKRTNIGMELITDPGILFLDEPTTGLDASTANAVLLLLKRMASQKGTIIFSIHQ 243

Qy      246 RYSIFKLFDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIINGDSTAV 305
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      244 RYSIFRLFDLTLAGRLLFHGSPSRDALDYFTGLGYECESHNNPADFFLDIINGDSTAV 303

Qy      306 ALNREEDFKATEIIEPSKQ-----DKPLIEKLAIEYVNSSFYKETKAELHQLSGGEKKKK 360
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      304 ALNKLED---VELENEQKEVDNDNGSKTVVENLSEQFCTTSYILETKAELEKMSLGKKIKS 360

Qy      361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVLGLVIGAIYFGLKNDS 420
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      361 NFFARQITYNTSFLHQLKWCKRSFKNLWRNPQASIAQVMVTLVLAIVGAIFFGVKEDV 420

Qy      421 TGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRYVSSYFLGKLLSDLLP 480
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      421 SGIQNRVGSFLFFVTTNQCFSSVSAIELFIVEKKIFIEHISGYRYLSAYFFAKLFTDLLP 480

Qy      481 MTMLPSIIFTICIVYFMLGLKPKADAFVMMFTLMMVAYSASSMALAIAAGQSVSVATLL 540
      | |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      481 MRTLPISIIFTSVIYFMIGFKATAGAFFTMMFTLMMIAYTAASSMALAVAAGQDVAVANLL 540

Qy      541 MTICFVFMMIFSGLLVNLTTIASWSLWLQYFSIPRYGFTALQHNEFLGQNFPCPLNAT-- 598
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      541 MTICFVFMIIFSGLLVNLTSVMDWISWLKYFSIPRYGLTALQINEFTNLNFCNGLNTTIQ 600

Qy      599 GNNPCN----YATCTGEEYLVKQGIDLSWPGLWKNHVALACMIVIFLTIAYLKLFLFKK 653
      || | : |||::|||::|||::|||::|||::|||::|||::|||::|||
Db      601 GNPCTGSSPFGTCTGEEYLVQGIDFSTWGLWQNHVALACMIAIFLTIAYLKLYFMKK 659

```

Search completed: September 18, 2008, 22:07:02

Job time : 414 secs

SCORE 2.0